

**Amendments to the Specification**

**Please amend the specification as follows:**

Please replace the paragraph beginning at page 7, line 13, with the following paragraph:

Figures 1A-C show a sequence comparison of *Thermus* DNA ligases.

Figure 1A illustrates the evolutionary tree for *Thermus* DNA ligases. Figure 1B is a regional sequence alignment of nine *Thermus* ligases: *Tsp. AK16D* (SEQ. ID. No. 22); *Thermus aquaticus YT-1* (SEQ. ID. No. 15); *Thermus Thermophilus* ("Tth") (SEQ. ID. No. 23); *Thermus flavus* (SEQ. ID. No. 16); *Thermus filiformis Tok4A2* (SEQ. ID. No. 17); *Thermus filiformis Tok6A1* (SEQ. ID. No. 18); *Tsp. SM32* (SEQ. ID. No. 19); *Tsp. Vil3* (SEQ. ID. No. 20); *T. scot* (SEQ. ID. No. 21). The aa (i.e. amino acid) sequence of *T. scot* retrieved from GenBank by accession number 1085749 (SEQ. ID. No. 31), is as follows:

Met	Thr	Leu	Glu	Glu	Ala	Arg	Lys	Arg	Val	Asn	Glu	Leu	Arg	Asp	Leu
1															15
Ile	Arg	Tyr	His	Asn	Tyr	Arg	Tyr	Tyr	Val	Leu	Ala	Asp	Pro	Glu	Ile
	20								25						30
Ser	Asp	Ala	Glu	Tyr	Asp	Arg	Leu	Leu	Arg	Glu	Leu	Lys	Glu	Leu	Glu
	35						40					45			
Glu	Arg	Phe	Pro	Glu	Leu	Lys	Ser	Pro	Asp	Ser	Pro	Thr	Glu	Gln	Val
	50					55					60				
Gly	Ala	Lys	Pro	Leu	Glu	Ala	Thr	Phe	Arg	Pro	Ile	Arg	His	Pro	Thr
	65				70			75							80
Arg	Met	Tyr	Ser	Leu	Asp	Asn	Ala	Phe	Asn	Phe	Asp	Glu	Leu	Lys	Ala
	85								90					95	
Phe	Glu	Glu	Arg	Ile	Gly	Arg	Ala	Leu	Gly	Arg	Glu	Cly	Pro	Phe	Ala
	100							105					110		
Tyr	Thr	Val	Glu	His	Lys	Val	Asp	Gly	Leu	Ser	Val	Asn	Leu	Tyr	Tyr
	115					120									125
Glu	Asp	Gly	Val	Leu	Val	Trp	Gly	Ala	Thr	Arg	Gly	Asp	Gly	Glu	Val
	130					135						140			
Gly	Glu	Glu	Val	Thr	Cln	Asn	Leu	Leu	Thr	Ile	Pro	Thr	Ile	Pro	Arg
	145						150				155				160
Arg	Val	Lys	Gly	Val	Pro	Glu	Arg	Leu	Glu	Val	Arg	Gly	Glu	Val	Tyr
	165							170						175	

Met Pro Ile Glu Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Lys  
 180 185 190

Gly Glu Lys Ile Phe Lys Asn Pro Arg Asn Ala Ala Gly Ser Leu  
 195 200 205

Arg Cln Lys Asp Pro Arg Ile Thr Ala Arg Arg Gly Leu Arg Ala Thr  
 210 215 220

Phe Tyr Ala Leu Gly Leu Gly Leu Glu Glu Ser Gly Leu Lys Thr Cln  
 225 230 235 240

Leu Asp Leu Leu His Trp Leu Arg Glu Lys Gly Phe Pro Val Glu His  
 245 250 255

Gly Phe Ala Arg Ala Glu Gly Ala Glu Gly Val Glu Arg Ile Tyr Cln  
 260 265 270

Gly Trp Leu Lys Glu Arg Arg Ser Leu Pro Phe Glu Ala Asp Gly Val  
 275 280 285

Val Val Lys Leu Asp Glu Leu Ser Leu Trp Arg Glu Leu Gly Tyr Thr  
 290 295 300

Ala Arg Ala Pro Arg Phe Ala Ile Ala Tyr Lys Phe Pro Ala Glu Glu  
 305 310 315 320

Lys Glu Thr Arg Leu Leu Cln Val Val Phe Cln Val Gly Arg Thr Gly  
 325 330 335

Arg Val Thr Pro Val Gly Ile Leu Glu Pro Val Phe Ile Glu Gly Ser  
 340 345 350

Val Val Ser Arg Val Thr Leu His Asn Glu Ser Tyr Ile Glu Glu Leu  
 355 360 365

Asp Val Arg Ile Gly Asp Trp Val Leu Val His Lys Ala Gly Gly Val  
 370 375 380

Ile Pro Glu Val Leu Arg Val Leu Lys Glu Lys Arg Thr Gly Glu Glu  
 385 390 395 400

Arg Pro Ile Arg Trp Pro Glu Thr Cys Pro Glu Cys Gly His Arg Leu  
 405 410 415

Val Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu Cys Pro Ala  
 420 425 430

Lys Arg Phe Glu Ala Ile Arg His Tyr Ala Ser Arg Lys Ala Met Asp  
 435 440 445

Ile Gly Gly Leu Gly Glu Lys Leu Ile Glu Lys Leu Leu Glu Lys Gly  
 450 455 460

Leu Val Lys Asp Val Ala Asp Leu Tyr Arg Leu Lys Lys Glu Asp Leu  
 465                    470                    475                    480  
 Leu Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Gln Asn Leu Leu Arg  
 485                    490                    495  
 Gln Ile Glu Glu Ser Lys Gly Arg Gly Leu Glu Arg Leu Leu Tyr Ala  
 500                    505                    510  
 Leu Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn Leu Ala Ala  
 515                    520                    525  
 His Phe Gly Thr Met Asp Arg Leu Leu Glu Ala Ser Leu Glu Glu Leu  
 530                    535                    540  
 Leu Gln Val Glu Glu Val Gly Glu Leu Thr Ala Arg Gly Ile Tyr Glu  
 545                    550                    555                    560  
 Thr Leu Gln Asp Pro Ala Phe Arg Asp Leu Val Arg Arg Leu Lys Glu  
 565                    570                    575  
 Ala Gly Val Val Met Glu Ala Lys Glu Arg Gly Glu Glu Ala Leu Lys  
 580                    585                    590  
 Gly Leu Thr Phe Val Ile Thr Gly Glu Leu Ser Arg Pro Arg Glu Glu  
 595                    600                    605  
 Val Lys Ala Leu Leu Arg Arg Leu Gly Ala Lys Val Thr Asp Ser Val  
 610                    615                    620  
 Ser Arg Lys Thr Ser Tyr Leu Val Val Gly Glu Asn Pro Gly Ser Lys  
 625                    630                    635                    640  
 Leu Glu Lys Ala Arg Ala Leu Gly Val Pro Thr Leu Thr Glu Glu Glu  
 645                    650                    655  
 Leu Tyr Arg Leu Ile Glu Glu Arg Thr Gly Lys Pro Val Glu Thr Leu  
 660                    665                    670  
 Ala Ser.

The adenylation motif KXDG (SEQ. ID. No. 24) is underlined and the adenylation site is marked by \*. The numbering of aa is based on *Tsp.* AK16D ligase (SEQ. ID. No. 1). Figure 1C is a complete amino acid sequence of *Tsp.* AK16D ligase (SEQ. ID. No. 1). The adenylation motif KXDG (SEQ. ID. No. 24) is underlined and the adenylation site <sup>118</sup>K is shown with a (\*) above the residue. The complete sequence of *Tsp.* AK16D ligase gene and partial sequences of six other *Thermus* ligase genes have been deposited with GenBank under accession No. AF092862 for *Tsp.* AK16D (SEQ. ID. No. 1), AF092863 for *Thermus aquaticus* YT-1 (SEQ. ID. No. 25), as follows:

Pro Glu Leu Lys Ser Pro Asp Ser Pro Thr Glu Cln Val Gly Ala Arg  
 1 5 10 15

Pro Leu Glu Ser Thr Phe Arg Pro Val Arg His Pro Thr Arg Met Tyr  
 20 25 30

Ser Leu Asp Asn Ala Phe Ser Leu Asp Glu Val Arg Ala Phe Glu Glu  
 35 40 45

Arg Ile Glu Arg Ala Leu Gly Arg Lys Gly Pro Phe Leu Tyr Thr Val  
 50 55 60

Glu His Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr Glu Glu Gly  
 65 70 75 80

Ile Leu Val Phe Gly Ala Thr Arg Gly Asp Gly Glu Thr Gly Glu Glu  
 85 90 95

Val Thr Cln Asn Leu Leu Thr Ile Arg Thr Ile Pro Arg Arg Leu Thr  
 100 105 110

Gly Val Pro Asp Arg Leu Glu Val Arg Gly Glu Val Tyr Met Pro Ile  
 115 120 125

Glu Ala Phe Leu Arg Leu Asn Cln Glu Leu Glu Glu Ala Gly Glu Arg  
 130 135 140

Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Cln Lys  
 145 150 155 160

Asp Pro Arg Val Thr Ala Arg Arg Gly Leu Arg Ala Thr Phe Tyr Ala  
 165 170 175

Leu Gly Leu Gly Leu Glu Glu Thr Gly Leu Lys Ser Cln His Asp Leu  
 180 185 190

Leu Leu Trp Leu Lys Glu Arg Gly Phe Pro Val Glu His Gly Phe Thr  
 195 200 205

Arg Ala Leu Gly Ala Glu Gly Val Glu Glu Val Tyr Cln Ala Trp Leu  
 210 215 220

Lys Glu Arg Arg Lys Leu Pro Phe Glu Ala Asp Gly Val Val Val Lys  
 225 230 235 240

Leu Asp Asp Leu Ala Leu Trp Arg Glu Leu Gly Tyr Thr Ala Arg Ala  
 245 250 255

Pro Arg Phe Ala Leu Ala Tyr Lys Phe Pro Ala Glu Glu Lys Glu Thr  
 260 265 270

Arg Leu Leu Ser Val Ala Phe Cln Val Gly Arg Thr Gly Arg Ile Thr  
 275 280 285

Pro Val Gly Val Leu Glu Pro Val Phe Ile Glu Gly Ser Glu Val Ser  
 290 295 300  
 Arg Val Thr Leu His Asn Glu Ser Phe Ile Glu Glu Leu Asp Val Arg  
 305 310 315 320  
 Ile Gly Asp Trp Val Leu Val His Lys Ala Gly Gly Val Ile Pro Glu  
 325 330 335  
 Val Leu Arg Val Leu Lys Glu Arg Arg Thr Gly Glu Glu Lys Pro Ile  
 340 345 350  
 Leu Trp Pro Glu Asn Cys Pro Glu Cys Gly His Ala Leu Leu Lys Glu  
 355 360 365  
 Gly Lys Val His Arg Cys Pro Asn Pro Leu Cys Pro Ala Lys Arg Phe  
 370 375 380  
 Glu Ala Ile Arg His Tyr Ala Ser Arg Lys Ala Met Asp Ile Gln Gly  
 385 390 395 400  
 Leu Gly Glu Lys Leu Ile Glu Lys Leu Leu Glu Lys Gly Leu Val Arg  
 405 410 415  
 Asp Val Ala Asp Leu Tyr Arg Leu Arg Lys Glu Asp Leu Leu Asp Leu  
 420 425 430  
 Glu Arg Met Gly Glu Lys Ser Ala Glu Asn Leu Leu Arg Gln Ile Glu  
 435 440 445  
 Glu Ser Lys Gly Arg Gly Leu Glu Arg Leu Leu Tyr Ala Leu Gly Leu  
 450 455 460  
 Pro Gly Val Gly Glu Val Leu Ala Arg Asn Leu Ala Leu Arg Phe Gly  
 465 470 475 480  
 His Met Asp Arg Leu Leu Glu Ala Gly Leu Gly Asp Leu Leu Glu Val  
 485 490 495  
 Glu Gly Val Gly Glu Leu Thr Ala Arg Ala Ile Leu Asn Thr Leu Lys  
 500 505 510  
 Asp Pro Glu Phe Arg Asp Leu Val Arg Arg Leu Lys Glu Ala Gly  
 515 520 525 ;

AF092864 for *Thermus flavus* (SEQ. ID. No. 26), as follows:

Arg Phe Pro Glu Leu Lys Ser Pro Asp Ser Pro Thr Glu Gln Val Gly  
 1 5 10 15  
 Ala Arg Pro Leu Glu Ala Thr Phe Arg Pro Val Arg His Pro Thr Arg  
 20 25 30

Met Tyr Ser Leu Asp Asn Ala Phe Asn Phe Asp Glu Leu Lys Ala Phe  
 35 40 45

Glu Glu Arg Ile Glu Arg Ala Leu Gly Arg Glu Gly Pro Phe Ala Tyr  
 50 55 60

Thr Val Glu His Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr Glu  
 65 70 75 80

Asp Gly Val Leu Val Tyr Gly Ala Thr Arg Gly Asp Gly Glu Val Gly  
 85 90 95

Glu Glu Val Thr Cln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg Arg  
 100 105 110

Leu Lys Gly Val Pro Glu Arg Leu Glu Val Arg Gly Glu Val Tyr Met  
 115 120 125

Pro Val Glu Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Arg Gly  
 130 135 140

Ala Arg Ile Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg  
 145 150 155 160

Gln Lys Asp Pro Arg Ile Thr Ala Lys Arg Gly Leu Arg Ala Thr Phe  
 165 170 175

Tyr Ala Leu Gly Leu Gly Leu Glu Val Glu Arg Glu Gly Val Ala  
 180 185 190

Thr Cln Phe Ala Leu Leu His Trp Leu Lys Glu Lys Ser Phe Pro Val  
 195 200 205

Glu His Gly Tyr Ala Arg Ala Val Gly Ala Glu Gly Val Glu Ala Val  
 210 215 220

Tyr Cln Asp Trp Leu Lys Lys Arg Arg Ala Leu Pro Phe Glu Ala Asp  
 225 230 235 240

Gly Val Val Val Lys Leu Asp Glu Leu Ala Leu Trp Arg Glu Leu Gly  
 245 250 255

Tyr Thr Ala Arg Ala Pro Arg Phe Ala Ile Ala Tyr Lys Phe Pro Ala  
 260 265 270

Glu Glu Lys Glu Thr Arg Leu Leu Asp Val Ala Phe Gln Val Gly Arg  
 275 280 285

Thr Gly Arg Val Thr Pro Val Gly Ile Leu Glu Pro Val Phe Leu Glu  
 290 295 300

Gly Ser Glu Val Ser Arg Val Thr Leu His Asn Glu Ser Tyr Ile Glu  
 305 310 315 320

Glu Leu Asp Ile Arg Ile Gly Asp Trp Val Leu Val His Lys Ala Gly  
 325 330 335

Gly Val Ile Pro Glu Val Leu Arg Val Leu Lys Glu Arg Arg Thr Gly  
 340 345 350

Glu Glu Arg Pro Ile Arg Trp Pro Glu Thr Cys Pro Glu Cys Gly His  
 355 360 365

Arg Leu Leu Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu Cys  
 370 375 380

Pro Ala Lys Arg Phe Glu Ala Ile Arg His Phe Pro Ser Arg Lys Ala  
 385 390 395 400

Met Asp Ile Cln Gly Leu Gly Glu Lys Leu Ile Glu Arg Leu Leu Glu  
 405 410 415

Lys Gly Leu Val Lys Asp Val Ala Asp Leu Tyr Arg Leu Arg Lys Glu  
 420 425 430

Asp Leu Val Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Cln Asn Leu  
 435 440 445

Leu Arg Cln Ile Glu Glu Ser Lys Arg Arg Gly Leu Glu Arg Leu Leu  
 450 455 460

Tyr Ala Leu Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn Leu  
 465 470 475 480

Ala Ala Arg Phe Gly Asn Met Asp Arg Leu Leu Glu Ala Ser Leu Glu  
 485 490 495

Glu Leu Leu Glu Val Glu Glu Val Gly Glu Leu Thr Ala Arg Ala Ile  
 500 505 510

Leu Glu Thr Leu Lys Asp Pro Ala Phe Arg Asp Leu Val Arg Arg Leu  
 515 520 525

Lys Glu Ala Gly Val Glu Met Glu Ala Lys Glu Lys Gly Gly Glu Ala  
 530 535 540

Leu Lys Gly Leu Thr Phe Val Ile Thr Gly Glu Leu Ser ;  
 545 550 555

AF092865 for *Thermus filiformis* Tok4A2 (SEQ. ID. No. 27), as follows:

Asp Ser Pro Thr Glu Cln Val Gly Ala Arg Pro Leu Glu Pro Thr Phe  
 1 5 10 15

Arg Pro Val Arg His Pro Thr Arg Met Tyr Ser Leu Asp Asn Ala Phe  
 20 25 30

Thr Tyr Glu Glu Val Leu Ala Phe Glu Glu Arg Leu Asp Arg Ala Leu  
 35 40 45

Gly Arg Lys Arg Pro Phe Leu Tyr Thr Val Glu His Lys Val Asp Gly  
 50 55 60

Leu Ser Val Asn Leu Tyr Tyr Glu Glu Gly Val Leu Val Phe Gly Ala  
 65 70 75 80

Thr Arg Gly Asp Xaa  
 85 90 95

Thr Ile Pro Thr Ile Pro Arg Arg Leu Lys Gly Val Pro Asp Arg Leu  
 100 105 110

Glu Val Arg Gly Glu Val Tyr Met Pro Ile Glu Ala Phe Leu Arg Leu  
 115 120 125

Asn Glu Glu Leu Glu Glu Arg Gly Glu Lys Val Phe Lys Asn Pro Arg  
 130 135 140

Asn Ala Ala Ala Gly Ser Leu Arg Gln Lys Asp Pro Arg Val Thr Ala  
 145 150 155 160

Lys Arg Gly Leu Arg Ala Thr Phe Tyr Ala Leu Gly Leu Gly Leu Glu  
 165 170 175

Glu Ser Gly Leu Lys Ser Gln Tyr Glu Leu Leu Leu Trp Leu Lys Glu  
 180 185 190

Lys Gly Phe Pro Val Glu His Gly Tyr Glu Lys Ala Leu Gly Ala Glu  
 195 200 205

Gly Val Glu Glu Val Tyr Gln Ala Xaa Xaa Xaa Lys Arg His Ala Leu  
 210 215 220

Pro Phe Glu Ala Asp Gly Val Val Lys Met Asp Asp Leu Thr Leu  
 225 230 235 240

Trp Gly Glu Leu Gly Tyr Thr Ala Arg Ala Pro Arg Phe Ala Ile Ala  
 245 250 255

Tyr Lys Phe Pro Ala Glu Glu Asn Glu Thr Arg Leu Leu Asp Val Asp  
 260 265 270

Phe Gln Val Gly Arg Thr Gly Arg Val Thr Pro Val Gly Ile Leu Glu  
 275 280 285

Pro Val Phe Leu Glu Gly Ser Glu Val Ser Arg Val Thr Leu His Asn  
 290 295 300

Glu Ser Tyr Ile Glu Glu Leu Asp Ile Arg Ile Gly Asp Trp Val Leu  
 305 310 315 320

Val His Lys Ala Gly Gly Val Ile Pro Glu Val Leu Arg Val Leu Lys  
 325 330 335

Glu Arg Arg Thr Gly Glu Glu Arg Pro Ile Arg Trp Pro Glu Thr Cys  
 340 345 350

Pro Glu Cys Gly His Arg Leu Leu Lys Glu Gly Lys Val His Arg Cys  
 355 360 365

Pro Asn Pro Leu Cys Pro Ala Lys Arg Phe Glu Ala Ile Arg His Phe  
 370 375 380

Pro Ser Arg Lys Ala Met Asp Ile Cln Gly Leu Gly Glu Lys Leu Ile  
 385 390 395 400

Glu Arg Leu Leu Glu Lys Gly Leu Val Lys Asp Val Ala Asp Leu Tyr  
 405 410 415

Arg Leu Arg Lys Glu Asp Leu Val Gly Leu Glu Arg Met Gly Glu Lys  
 420 425 430

Ser Ala Cln Asn Leu Leu Arg Cln Ile Glu Glu Ser Lys Arg Arg Gly  
 435 440 445

Leu Glu Arg Leu Leu Tyr Ala Leu Gly Leu Pro Gly Val Gly Glu Val  
 450 455 460

Leu Ala Arg Asn Leu Ala Ala Arg Phe Gly Asn Met Asp Arg Leu Leu  
 465 470 475 480

Glu Ala Ser Leu Glu Glu Leu Leu Glu Val Glu Glu Val Gly Glu Leu  
 485 490 495

Thr Ala Arg Ala Ile Leu Glu Thr Leu Lys Asp Pro Ala Phe Arg Asp  
 500 505 510

Leu Val Arg Arg Leu Lys Glu Ala Gly Val Glu Met Gly Ala Lys Glu  
 515 520 525

Lys Gly Gly Glu Ala Leu Lys Gly Leu Thr Phe Val Ile Thr Gly Glu  
 530 535 540

Leu Ser  
 545 ;

AF092866 for *Thermus filiformis* Tok6A1 (SEQ. ID. No. 28), as follows:

Arg Phe Pro Glu Phe Lys Ser Pro Asp Ser Pro Thr Glu Cln Val Gly  
 1 5 10 15

Ala Arg Pro Leu Glu Pro Thr Phe Arg Pro Val Arg His Pro Thr Arg  
 20 25 30

Met Tyr Ser Leu Asp Asn Ala Phe Thr Tyr Glu Glu Val Leu Ala Phe  
 35 40 45

Glu Glu Arg Leu Glu Arg Ala Leu Gly Arg Lys Arg Pro Phe Leu Tyr  
 50 55 60

Thr Val Glu His Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr Glu  
 65 70 75 80

Glu Gly Val Leu Val Phe Gly Ala Thr Arg Gly Asp Gly Glu Val Gly  
 85 90 95

Glu Glu Val Thr Cln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg Arg  
 100 105 110

Leu Lys Gly Val Pro Asp Arg Leu Glu Val Arg Gly Glu Val Tyr Met  
 115 120 125

Pro Ile Glu Ala Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Arg Gly  
 130 135 140

Glu Lys Val Phe Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg  
 145 150 155 160

Cln Lys Asp Pro Arg Val Thr Ala Lys Arg Gly Leu Arg Ala Thr Phe  
 165 170 175

Tyr Ala Leu Gly Leu Gly Leu Glu Ser Gly Leu Lys Ser Cln Tyr  
 180 185 190

Glu Leu Leu Leu Trp Leu Lys Glu Lys Gly Phe Pro Val Glu His Gly  
 195 200 205

Tyr Glu Lys Ala Leu Gly Ala Glu Gly Val Glu Glu Val Tyr Arg Arg  
 210 215 220

Phe Leu Ala Cln Arg His Ala Leu Pro Phe Glu Ala Asp Gly Val Val  
 225 230 235 240

Val Lys Leu Asp Asp Leu Ala Leu Trp Arg Glu Leu Gly Tyr Thr Ala  
 245 250 255

Arg Ala Pro Arg Phe Ala Leu Ala Tyr Lys Phe Pro Ala Glu Glu Lys  
 260 265 270

Glu Thr Arg Leu Leu Asp Val Val Phe Cln Val Gly Arg Thr Gly Arg  
 275 280 285

Val Thr Pro Val Gly Val Leu Glu Pro Val Phe Ile Glu Gly Ser Glu  
 290 295 300

Val Ser Arg Val Thr Leu His Asn Glu Ser Tyr Ile Glu Glu Leu Asp  
 305 310 315 320

Ile Arg Ile Gly Asp Trp Val Leu Val His Lys Ala Gly Gly Val Ile  
 325 330 335  
 Pro Glu Val Leu Arg Val Leu Lys Glu Arg Arg Thr Gly Glu Glu Arg  
 340 345 350  
 Pro Ile Arg Trp Pro Glu Thr Cys Pro Glu Cys Gly His Arg Leu Val  
 355 360 365  
 Lys Glu Gly Lys Val His Arg Cys Pro Asn Pro Leu Cys Pro Ala Lys  
 370 375 380  
 Arg Phe Glu Ala Ile Arg His Tyr Ala Ser Arg Lys Ala Met Asp Ile  
 385 390 395 400  
 Glu Gly Leu Gly Glu Lys Leu Ile Glu Arg Leu Leu Glu Lys Gly Leu  
 405 410 415  
 Val Arg Asp Val Ala Asp Leu Tyr His Leu Arg Lys Glu Asp Leu Leu  
 420 425 430  
 Gly Leu Glu Arg Met Gly Glu Lys Ser Ala Cln Asn Leu Leu Arg Cln  
 435 440 445  
 Ile Glu Glu Ser Lys His Arg Gly Leu Glu Arg Leu Leu Tyr Ala Leu  
 450 455 460  
 Gly Leu Pro Gly Val Gly Glu Val Leu Ala Arg Asn Leu Ala Arg Arg  
 465 470 475 480  
 Phe Gly Thr Met Asp Arg Leu Leu Glu Ala Ser Leu Glu Glu Leu Leu  
 485 490 495  
 Glu Val Glu Glu Val Gly Glu Leu Thr Ala Arg Ala Ile Leu Glu Thr  
 500 505 510  
 Leu Lys Asp Pro Ala Phe Arg Asp Leu Val Arg Arg Leu Lys Glu Ala  
 515 520 525  
 Gly Val Ser Met Glu Ser Lys Glu Glu  
 530 535 ;

AF092867 for *Tsp. Vil3* (SEQ. ID. No. 29), as follows:

Pro Ser Pro Asp Ser Pro Thr Glu Cln Val Gly Ala Lys Pro Leu Glu  
 1 5 10 15  
 Ala Thr Phe Arg Pro Ile Arg His Pro Thr Arg Met Tyr Ser Leu Asp  
 20 25 30  
 Asn Ala Phe Thr Leu Glu Glu Val Arg Thr Phe Glu Glu Arg Ile Glu  
 35 40 45

Arg Ala Leu Gly Arg Lys Gly Pro Phe Val Tyr Thr Val Glu His Lys  
 50 55 60

Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr Glu Glu Gly Ile Leu Val  
 65 70 75 80

Trp Gly Ala Thr Arg Gly Asp Gly Glu Thr Gly Glu Glu Val Thr Gln  
 85 90 95

Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg Arg Leu Lys Gly Val Pro  
 100 105 110

Glu Arg Leu Glu Val Arg Gly Glu Val Tyr Met Pro Ile Glu Ala Phe  
 115 120 125

Leu Arg Leu Asn Glu Glu Leu Glu Glu Lys Gly Glu Lys Ile Phe Lys  
 130 135 140

Asn Pro Arg Asn Ala Ala Gly Ser Phe Arg Gln Lys Asp Pro Arg  
 145 150 155 160

Ile Thr Ala Arg Arg Gly Leu Arg Ala Thr Phe Tyr Ala Leu Gly Leu  
 165 170 175

Gly Leu Glu Glu Ser Gly Leu Lys Thr Gln Leu Asp Leu Leu His Trp  
 180 185 190

Leu Arg Glu Lys Gly Phe Pro Val Glu His Gly Phe Ala Arg Ala Glu  
 195 200 205

Gly Ala Glu Gly Val Glu Arg Ile Tyr Gln Gly Trp Leu Lys Glu Arg  
 210 215 220

Arg Ser Leu Pro Phe Glu Ala Asp Gly Val Val Val Lys Leu Asp Glu  
 225 230 235 240

Leu Ser Leu Trp Arg Glu Leu Gly Tyr Thr Ala Arg Ala Pro Arg Phe  
 245 250 255

Ala Ile Ala Tyr Lys Phe Pro Ala Glu Glu Lys Glu Thr Ala Leu Phe  
 260 265 270

Gln Val Val Leu Gln Val Gly Arg Thr Gly Gln Val Thr Pro Val Gly  
 275 280 285

Ile Leu Glu Pro Val Phe Ile Glu Gly Ser Glu Val Ser Arg Val Thr  
 290 295 300

Leu His Asn Glu Ser Tyr Ile Glu Asp Leu Asp Val Arg Ile Gly Glu  
 305 310 315 320

Trp Val Leu Val His Asn Ala Gly Gly Val Ile Pro Glu Val Leu Arg  
 325 330 335

Val Leu Lys Glu Lys Arg Thr Gly Glu Glu Arg Pro Ile Arg Trp Pro  
 340 345 350  
 Glu Thr Cys Pro Glu Cys Gly His Arg Leu Val Lys Glu Gly Lys Val  
 355 360 365  
 His Arg Cys Pro Asn Pro Leu Cys Pro Ala Lys Arg Phe Glu Ala Ile  
 370 375 380  
 Arg His Tyr Ala Ser Arg Lys Ala Met Asp Ile Gly Gly Leu Gly Glu  
 385 390 395 400  
 Lys Leu Ile Glu Lys Leu Leu Glu Lys Gly Leu Val Lys Asp Val Ala  
 405 410 415  
 Asp Leu Tyr Arg Leu Lys Glu Glu Asp Leu Val Gly Leu Glu Arg Met  
 420 425 430  
 Gly Lys Lys Ser Ala Cln Asn Leu Leu Arg Cln Ile Glu Lys Ser Lys  
 435 440 445  
 Ala Arg Gly Leu Glu Arg Leu Leu Tyr Ala Leu Gly Leu Pro Gly Val  
 450 455 460  
 Gly Glu Val Leu Ala Arg Asn Leu Ala Ala His Phe Gly Thr Met Asp  
 465 470 475 480  
 Arg Leu Leu Glu Ala Ser Leu Glu Glu Leu Leu Cln Val Glu Glu Val  
 485 490 495  
 Gly Glu Leu Thr Ala Arg Gly Ile Tyr  
 500 505;

and AF092868 for *Tsp. SM32* (SEQ. ID. No. 30), as follows:

Asp Asn Ala Phe Thr His His Asp Leu Lys Ala Phe Glu Asp Arg Val  
 1 5 10 15  
 Asp Arg Ala Leu Gly Arg Glu Gly Pro Phe Val Tyr Thr Val Glu His  
 20 25 30  
 Lys Val Asp Gly Leu Ser Val Asn Leu Tyr Tyr Glu Glu Gly Ile Leu  
 35 40 45  
 Val Phe Gly Ala Pro Arg Gly Asp Gly Glu Val Gly Glu Glu Val Thr  
 50 55 60  
 Cln Asn Leu Leu Thr Ile Pro Thr Ile Pro Arg Arg Leu Lys Gly Val  
 65 70 75 80  
 Pro Glu Arg Leu Glu Val Arg Gly Glu Val Tyr Met Pro Ile Glu Ala  
 85 90 95

Phe Leu Arg Leu Asn Glu Glu Leu Glu Glu Ala Gly Glu Lys Val Phe  
 100 105 110

Lys Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Cln Lys Asp Pro  
 115 120 125

Arg Ile Thr Ala Lys Arg Gly Leu Arg Ala Thr Phe Tyr Ala Leu Gly  
 130 135 140

Leu Gly Leu Glu Glu Ser Gly Leu Lys Thr Cln Tyr Glu Phe Leu Leu  
 145 150 155 160

Trp Phe Lys Glu Lys Gly Phe Pro Val Glu His Gly Phe Ala Arg Ala  
 165 170 175

Thr Gly Ala Glu Gly Val Glu Arg Val Tyr Cln Gly Trp Leu Gln Lys  
 180 185 190

Arg Arg Lys Leu Pro Phe Glu Ala Asp Gly Val Val Val Lys Leu Asp  
 195 200 205

Glu Leu Ala Leu Trp Arg Glu Leu Gly Tyr Thr Ala Arg Ala Pro Arg  
 210 215 220

Phe Ala Ile Ala Tyr Lys Phe Pro Ala Glu Glu Lys Glu Thr Arg Leu  
 225 230 235 240

Leu Asp Val Val Phe Cln Val Gly Arg Thr Gly Arg Val Thr Pro Val  
 245 250 255

Gly Ile Leu Glu Pro Val Leu Ile Glu Gly Ser Glu Val Ser Arg Val  
 260 265 270

Thr Leu His Asn Glu Ser Tyr Ile Glu Glu Leu Asp Ile Arg Ile Gly  
 275 280 285

Asp Trp Val Leu Val His Lys Ala Gly Gly Val Ile Pro Glu Val Leu  
 290 295 300

Arg Val Leu Lys Glu Arg Arg Thr Gly Ala Glu Arg Pro Ile Val Trp  
 305 310 315 320

Pro Glu Asn Cys Pro Glu Cys Gly His His Leu Val Lys Glu Gly Lys  
 325 330 335

Val His Arg Cys Pro Asn Pro Leu Cys Pro Ala Lys Arg Phe Glu Ala  
 340 345 350

Ile Arg His Tyr Ala Ser Arg Lys Ala Met Asp Ile Gln Gly Leu Gly  
 355 360 365

Glu Lys Leu Ile Glu Lys Leu Leu Glu Asn Gly Leu Val Lys Asp Val  
 370 375 380

Ala Asp Leu Tyr Arg Leu Arg Lys Glu Asp Leu Val Gly Leu Glu Arg  
385 390 395 400

Met Gly Glu Lys Ser Ala Glu Asn Leu Leu Arg Gln Ile Glu Glu Ser  
405 410 415

Lys His Arg Gly Leu Glu Arg Leu Leu Tyr Ala Leu Gly Leu Pro Gly  
420 425 430

Val Gly Glu Val Leu Ala Arg Asn Leu Ala Ala Arg Phe Gly Thr Met  
435 440 445

Asp Arg Leu Leu Glu Ala Thr Leu Glu Glu Leu Leu Glu Val Glu Glu  
450 455 460

Val Gly Glu Leu Thr Ala Arg Gly Ile Trp Glu Thr Leu Gln Asp Pro  
465 470 475 480

Ala.